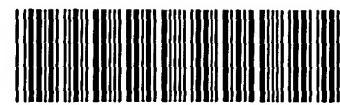


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#10



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,467

DATE: 07/02/2002

TIME: 14:04:49

Input Set : N:\Crf3\RULE60\10057467.raw
 Output Set: N:\CRF3\07022002\J057467.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Nolan, Garry P.
 6 Rothenberg, Michael S.

8 (ii) TITLE OF INVENTION: Methods for Screening for Transdominant
 9 Effector Peptides and RNA Molecules

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 15 (B) STREET: 4 Embarcadero Center, Suite 3400
 16 (C) CITY: San Francisco
 17 (D) STATE: CA
 18 (E) COUNTRY: USA
 19 (F) ZIP: 94111-4187

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk
 23 (B) COMPUTER: IBM PC compatible
 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

ENTERED

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/057,467
 C--> 29 (B) FILING DATE: 22-Jan-2002
 30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/589,109
 34 (B) FILING DATE: 23-JAN-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Silva, Robin M.
 40 (B) REGISTRATION NUMBER: 38,304
 41 (C) REFERENCE/DOCKET NUMBER: A-64259/DJB/RMS

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (415) 781-1989
 45 (B) TELEFAX: (415) 949-8711

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 9 amino acids
 51 (B) TYPE: amino acid
 52 (C) STRANDEDNESS:

W--> 53 (D) TOPOLOGY: Not Relevant

55 (ii) MOLECULE TYPE: peptide

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 59 Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa

60 1 5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,467

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Input Set : N:\Crf3\RULE60\10057467.raw
 Output Set: N:\CRF3\07022002\J057467.raw

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62 (2) INFORMATION FOR SEQ ID NO: 2:
64   (i) SEQUENCE CHARACTERISTICS:
65     (A) LENGTH: 92 base pairs
66     (B) TYPE: nucleic acid
67     (C) STRANDEDNESS: double
68     (D) TOPOLOGY: linear
70   (ii) MOLECULE TYPE: cDNA
72   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74 GCTTAGCAAG ATCTCTACGG TGGACCKNNK NNKNNKNNKN NKNNKNNKNN KNNKNNCCCC      60
76 ACTCCCATGG TCCTACGTAC CACCACACTG GG
78 (2) INFORMATION FOR SEQ ID NO: 3:
80   (i) SEQUENCE CHARACTERISTICS:
81     (A) LENGTH: 34 base pairs
82     (B) TYPE: nucleic acid
83     (C) STRANDEDNESS: double
84     (D) TOPOLOGY: linear
86   (ii) MOLECULE TYPE: cDNA
88   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89 GCTTAGCAAG ATCTGTGT CAGTTAGGGT GTGG
90 GCTTAGCAAG ATCTGTGT CAGTTAGGGT GTGG
92 (2) INFORMATION FOR SEQ ID NO: 4:
94   (i) SEQUENCE CHARACTERISTICS:
95     (A) LENGTH: 74 base pairs
96     (B) TYPE: nucleic acid
97     (C) STRANDEDNESS: double
98     (D) TOPOLOGY: linear
100  (ii) MOLECULE TYPE: cDNA
102  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
104 CTGGAGAACCTT AGGACCATGG GCNNKNNKNN KNKNNKNNKN NKNNKNNKNN NKGGGCC
106 TTAAACCATT AAAT
108 (2) INFORMATION FOR SEQ ID NO: 5:
110  (i) SEQUENCE CHARACTERISTICS:
111    (A) LENGTH: 71 base pairs
112    (B) TYPE: nucleic acid
113    (C) STRANDEDNESS: double
114    (D) TOPOLOGY: linear
116  (ii) MOLECULE TYPE: cDNA
118  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
119 CTGGAGAACCTT AGGACCATGG GCNNKNNKNN KCCTCCCNK CCTNNKNNKG GGCCCCCTTA
120 CTGGAGAACCTT AGGACCATGG GCNNKNNKNN KCCTCCCNK CCTNNKNNKG GGCCCCCTTA      60
122 AACCATAAA T
124 (2) INFORMATION FOR SEQ ID NO: 6:
126  (i) SEQUENCE CHARACTERISTICS:
127    (A) LENGTH: 26 base pairs
128    (B) TYPE: nucleic acid
129    (C) STRANDEDNESS: double
130    (D) TOPOLOGY: linear
132  (ii) MOLECULE TYPE: cDNA
134  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
135 TCATGCATCC AATTAAATGG TTTAAG
136 TCATGCATCC AATTAAATGG TTTAAG
138 (2) INFORMATION FOR SEQ ID NO: 7:

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RAW SEQUENCE LISTING
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Output Set: N:\CRF3\07022002\J057467.raw

140	(i) SEQUENCE CHARACTERISTICS:	
141	(A) LENGTH: 4950 base pairs	
142	(B) TYPE: nucleic acid	
143	(C) STRANDEDNESS: double	
144	(D) TOPOLOGY: linear	
146	(ii) MOLECULE TYPE: DNA (genomic)	
148	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
150	TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCAT	60
152	GGAAAATACA TAACTGAGAA TAGAGAACCTT CAGATCAAGG TTAGGAACAG AGAGACAGCA	120
154	GAATATGGGC CAAACAGGAT ATCTGTGGTA AGCAGTTCT GCCCCGGCTC AGGGCCAAGA	180
156	ACAGATGGTC CCCAGATGCG GTCCCCCCT CAGCAGTTTC TAGAGAACCA TCAGATGTTT	240
158	CCAGGGTGCC CCAAGGACCT GAAAATGACC CTGTGCCCTTA TTTGAACCTAA CCAATCAGTT	300
160	CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC TCCCCGAGCT CAATAAAAGA GCCCACAAACC	360
162	CCTCACTCGG CGGCCAGTC CTCCGATAGA CTGCGTCGCC CGGGTACCCG TATTCCAAT	420
164	AAAGCCTCTT GCTGTTGCA TCCGAATCGT GGACTCGCTG ATCCTTGGGA GGGTCTCCTC	480
166	AGATTGATTG ACTGCCAACCC TCGGGGGTCT TTCATTTGGA GGTTCCACCG AGATTTGGAG	540
168	ACCCCTGCCT AGGGACCACCC GACCCCCCG CGGGGAGGTA AGCTGGCCAG CGGTCGTTTC	600
170	CTGTCTGTCT CTGTCTTTGT GCGTGTGTTGT GCGGGCATCT AATGTTGCG CCTGCGTCTG	660
172	TACTAGTTAG CTAACATAGCT CTGTATCTGG CGGACCCGTG GTGGAACCTGA CGAGTTCTGA	720
174	ACACCCGGCC GCAACCCCTGG GAGACGTCCC AGGGACTTTG GGGGCGCTTT TTGTGGCCCG	780
176	ACCTGAGGAA GGGAGTCGAT GTGGAATCCG ACCCCGTCAG GATATGTGTT TCTGGTAGGA	840
178	GACGAGAACCC TAAAACAGTT CCCGCCTCCG TCTGAATTT TGCTTTCGGT TTGGAACCGA	900
180	AGCCGCGCGT CTTGTCGTGC GCAGCGCTGC AGCATCGTTC TGTGTTCTCT CTGTCGACT	960
182	GTGTTTCTGT ATTGTCGTGA AAATTAGGGC CAGACTGTTA CCACTCCCTT AAGTTTGACC	1020
184	TTAGGTCACT GGAAAAGATGT CGAGCGGATC GCTCACAAAC AGTCGGTAGA TGTCAAGAAC	1080
186	AGACGTTGGG TTACCTTCGT CTCTGCAGAA TGGCCAACCT TTAACGTCGG ATGGCCGCGA	1140
188	GACGGCACCT TAAACCGAGA CCTCATCAC CAGGTTAAGA TCAAGGTCTT TTCACCTGGC	1200
190	CCGCATGGAC ACCCAGACCA GGTCCCCCTAC ATCGTGACCT GGGAAGCCTT GGCTTTGAC	1260
192	CCCCCTCCCT GGGTCAAGCC CTTTGTACAC CCTAAGCCTC CGCCTCCTCT TCCTCCATCC	1320
194	GCCCCGTCTC TCCCCCTTGA ACCTCCTCGT TCGACCCCCGC CTCGATCCCTC CCTTTATCCA	1380
196	GCCCTCACTC CTTCTCTAGG CGCCGGAATT CCAGGACCAT GGGCGGGCCC CCTTAAACCA	1440
198	TTAAATTGGT AAAATAAAGG ATCCGTCGAC CTGCAAGCCAA GCTTATCGAT AAAATAAAG	1500
200	ATTTTATTTA GTCTCCAGAA AAAGGGGGGA ATGAAAAGACC CCACCTGTAG GTTTGGCAAG	1560
202	CTAGCTTAAG TAAAGCCATT TTGCAAGGCA TGGAAAATAC ATAACGTGAGA ATAGAGAAC	1620
204	TCAGATCAAG GTAGGAACA GAGAGACAGC AGAATATGGG CCAAACAGGA TATCTGTGGT	1680
206	AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG AACAGATGGT CCCCAGATGC GGTCCCGCCC	1740
208	TCAGCAGTTT CTAGAGAACCC ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAAATGAC	1800
210	CCTGTGCCCTT ATTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG CGCGCTTCTG	1860
212	CTCCCCGAGC TCAATAAAAG AGCCCACAAAC CCCTCACTCG GCGCGCCAGT CCTCCGATAG	1920
214	ACTGCGTCGC CGGGGTACCC GTGTATCCAA TAAACCCCTCT TGCAAGGTGCA TCCGACTTGT	1980
216	GGTCTCGCTG TTCTTGGGA GGGTCTCCTC TGAGTGATTG ACTACCCGTC AGCAGGGGTC	2040
218	TTTCATTGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAAATT	2100
220	CCACACAAACA TACCGAGCCGG AAGCATAAAG TGTAAAGCCT GGGGTGCCTA ATGAGTGAGC	2160
222	TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTCTC AGTCGGGAAA CCTGTCGTGC	2220
224	CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGGCG GTTGTGCGTAT TGGGCCTCT	2280
226	TCCGCTCCCT CGCTCACTGA CTCGCTGCAGC TCGGTGCGTC GGCTGCGGGCG AGCGGTATCA	2340
228	GCTCACTCAA AGGGCGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC	2400
230	ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT	2460
232	TTCCATAGGC TCCGCCCGCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG	2520

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234	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTCCCC	CTGGAAGCTC	CCTCGTGC	2580
236	TCTCCTGTC	CGACCCCTGCC	GCTTACCGA	TACCTGTCCG	CCTTCTCCC	TTCGGGAA	2640
238	GTGGCGCTT	CTCATAGCTC	ACGCTGTAGG	TATCTCAGTT	CGGTGTAGGT	CGTTCGCT	2700
240	AAGCTGGGCT	GTGTGCACGA	ACCCCCCGTT	CAGCCCGACC	GCTGCGCTT	ATCCGGTAAC	2760
242	TATCGTCTT	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	CACTGGCAGC	AGCCACTGGT	2820
244	AACAGGATT	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	AGTTCTGAA	GTGGTGGC	2880
246	AACTACGGCT	ACACTAGAAC	GACAGTATT	GGTATCTGCG	CTCTGCTGAA	GCCAGTTACC	2940
248	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	CCACCGCTGG	TAGCGGTGGT	3000
250	TTTTTTGTTT	GCAAGCAGCA	GATTACGCG	AGAAAAAAAG	GATCTCAAGA	AGATCCTTG	3060
252	ATCTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAA	CACGTTAAGG	GATTTGGTC	3120
254	ATGAGATTAT	CAAAAGGAT	CTTCACCTAG	ATCCTTTAA	ATTAAGGAT	AAGTTTAAA	3180
256	TCAATCTAAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	ACCAATGCTT	AATCAGTGAG	3240
258	GCACCTATCT	CAGCGATCTG	TCTATTCGT	TCATCCATAG	TTGCGTGA	CCCCGTCGT	3300
260	TAGATAACTA	CGATACGGGA	GGGCTTACCA	TCTGGCCCA	GTGCTGCAAT	GATACCGCGA	3360
262	GACCCACGCT	CACCGGCTCC	AGATTTATCA	GCAATAAAC	AGCCAGCCGG	AAGGGCCGAG	3420
264	CGCAGAAGTG	GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	CTATTAAATTG	TTGCGGGAA	3480
266	GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	TTGTTGCCAT	TGCTACAGGC	3540
268	ATCGTGGTGT	CACGCTCGTC	GTGGTATG	GCTTCATTCA	GCTCCGGTTC	CCAACGATCA	3600
270	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	AAAAAAGCGG	TTAGCTCCTT	CGGTCCCTCCG	3660
272	ATCGTTGTCA	GAAGTAAGTT	GGCCGCAGTG	TTATCACTCA	TGGTTATGGC	AGCACTGCAT	3720
274	AATTCTCTTA	CTGTCATGCC	ATCCGTAAGA	TGCTTTCTG	TGACTGGTGA	GTACTCAACC	3780
276	AAGTCATTCT	GAGAATAGTG	TATGCGGCCG	CCGAGTTGCT	CTTGGCCCGC	GTCAATAACGG	3840
278	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGTCA	TCATTGGAAA	ACGTTCTCG	3900
280	GGGCGAAAAC	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	TTGCGATGTA	ACCCACTCGT	3960
282	GCACCCAAC	GATCTTCAGC	ATCTTTACT	TTCACCAAGCG	TTTCTGGGTG	AGCAAAACA	4020
284	GGAAGGCCAA	ATGCCGCAA	AAAGGGAATA	AGGGCGACAC	GGAAATGTTG	AATACTCATA	4080
286	CTCTTCCTT	TTCAATATTA	TTGAAAGCATT	TATCAGGGTT	ATTGTCTCAT	GAGGGATAC	4140
288	ATATTGAAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTT	CGCGCACATT	TCCCCGAAA	4200
290	GTGCCACCTG	ACGTCTAAGA	AACCATTATT	ATCATGACAT	TAACCTATAA	AAATAGGC	4260
292	ATCACGAGGC	CCTTCGTC	CGCGCGTTTC	GGTGATGACG	GTAAAACCT	CTGACACATG	4320
294	CAGCTCCCGG	AGACGGTCAC	AGCTTGTCTG	TAAGCGGATG	CCGGGAGCAG	ACAAGCCGT	4380
296	CAGGGCGCGT	CAGCGGGTGT	TGGCGGGTGT	CGGGGCTGGC	TAAACTATGC	GGCATCAGAG	4440
298	CAGATTGTAC	TGAGAGTGCA	CCATATGCCG	TGTGAAATAC	CGCACAGATG	CGTAAGGAGA	4500
300	AAATACCGCA	TCAGGCCCA	TTCGCCATT	AGGCTGCGCA	ACTGTTGGGA	AGGGCGATCG	4560
302	GTGCGGGCCT	CTTCGCTATT	ACGCCAGCTG	GCGAAAGGGG	GATGTGCTGC	AAGGGGATTA	4620
304	AGTTGGTAA	CGCCAGGGTT	TTCCCAGTC	CGACGTTGTA	AAACGACGGC	CAGTGCCACG	4680
306	CTCTCCCTTA	TGCGACTCCT	GCATTAGGAA	GCAGCCAGT	AGTAGGTTGA	GGCCGTTGAG	4740
308	CACCGCCGCC	GCAAGGAATG	GTGCATGCAA	GGAGATGGCG	CCCAACAGTC	CCCCGGCCAC	4800
310	GGGGCCTGCC	ACCATACCCA	CGCCGAAACA	AGCGCTCATG	AGCCCGAAGT	GGCGAGCCCG	4860
312	ATCTTCCCCA	TGGGTGATGT	CGGCGATATA	GGGCCAGCA	ACCGCACCTG	TGGGCCGGT	4920
314	GATGCCGCC	ACGATGCGTC	CGGCGTAGAG				4950

316 (2) INFORMATION FOR SEQ ID NO: 8:

318 (i) SEQUENCE CHARACTERISTICS:

319 (A) LENGTH: 7 amino acids

320 (B) TYPE: amino acid

321 (C) STRANDEDNESS:

W--> 322 (D) TOPOLOGY: Not Relevant

324 (ii) MOLECULE TYPE: peptide

326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/057,467

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Input Set : N:\Crf3\RULE60\10057467.raw
 Output Set: N:\CRF3\07022002\J057467.raw

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328     Pro Lys Lys Lys Arg Lys Val
329         1             5
331 (2) INFORMATION FOR SEQ ID NO: 9:
333     (i) SEQUENCE CHARACTERISTICS:
334         (A) LENGTH: 20 amino acids
335         (B) TYPE: amino acid
336         (C) STRANDEDNESS:
W--> 337         (D) TOPOLOGY: Not Relevant
339     (ii) MOLECULE TYPE: peptide
341     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
343     Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
344     1             5             10            15
346     Lys Lys Leu Asp
347             20
349 (2) INFORMATION FOR SEQ ID NO: 10:
351     (i) SEQUENCE CHARACTERISTICS:
352         (A) LENGTH: 4 amino acids
353         (B) TYPE: amino acid
354         (C) STRANDEDNESS:
W--> 355         (D) TOPOLOGY: Not Relevant
357     (ii) MOLECULE TYPE: peptide
359     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
361     Gly Gly Pro Pro
362     1
364 (2) INFORMATION FOR SEQ ID NO: 11:
366     (i) SEQUENCE CHARACTERISTICS:
367         (A) LENGTH: 48 base pairs
368         (B) TYPE: nucleic acid
369         (C) STRANDEDNESS: unknown
370         (D) TOPOLOGY: unknown
372     (ii) MOLECULE TYPE: cDNA
374     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
376 ATGGGAAAGA AGAAGAAGAA GAAGAAGAAG AAGAAGGGGG GGCCCCCCC
378 (2) INFORMATION FOR SEQ ID NO: 12:
380     (i) SEQUENCE CHARACTERISTICS:
381         (A) LENGTH: 30 base pairs
382         (B) TYPE: nucleic acid
383         (C) STRANDEDNESS: unknown
384         (D) TOPOLOGY: unknown
386     (ii) MOLECULE TYPE: cDNA
388     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
390 CCTCCCTCCTC CTCCCTCCTC TCCTCCCTCCT
392 (2) INFORMATION FOR SEQ ID NO: 13:
394     (i) SEQUENCE CHARACTERISTICS:
395         (A) LENGTH: 30 base pairs
396         (B) TYPE: nucleic acid
397         (C) STRANDEDNESS: unknown
398         (D) TOPOLOGY: unknown
400     (ii) MOLECULE TYPE: cDNA

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30

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/02/2002
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Input Set : N:\Crf3\RULE60\10057467.raw
Output Set: N:\CRF3\07022002\J057467.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.1,2,3,6,8,9
Seq#:2; N Pos. 28,29,31,32,34,35,37,38,40,41,43,44,46,47,49,50,52,53,55,56
Seq#:4; N Pos. 23,24,26,27,29,30,32,33,35,36,38,39,41,42,44,45,47,48,50,51
Seq#:5; N Pos. 23,24,26,27,29,30,38,39,44,45,47,48
Seq#:13; N Pos. 3,6,9,12,15,18,21,24,27,30
Seq#:14; N Pos. 3,6,9,12,15,18,21,24,27,30

VERIFICATION SUMMARY

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Output Set: N:\CRF3\07022002\J057467.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:53 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:322 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:337 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:355 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10